

10/584024

SEQUENCE LISTING

JAP20 Rec'd PCI/PTO 22 JUN 2006

<110> CropDesign N.V.

<120> Plants having increased yield and method for making the same

<130> 1187-31

<150> PCT/EP2004/053683

<151> 2004-12-22

<150> US 60/532,287

<151> 2003-12-22

<160> 5

<170> PatentIn version 3.3

<210> 1

<211> 1311

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<223> A variant of the coding sequence of the sequence deposited under accession number NM_121168 contains a G instead of C on position 851 and a T instead of C on position 1295

<400> 1

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gtacaggaga gtttgcgtacg aataacgaga tcacgagcta aaaaagccat ggaaagagga 120

gtatcaatac ctccaacaaa accttctttt aaacagcaaa agagacgtgc agtacttaag 180

gatgtgagta atacctctgc agatattatt tattcagaac ttcaaggg aggcaacatc 240

aaggcaaaca gaaaatgtct aaaagagcct aaaaaagcag caaaggaagg tgctaacagt 300

gccatggata ttctggtaga tatgcataca gaaaaatcaa aattagcaga agatttgtcc 360

aagatcagga tggctgaagc ccaagatgtc tctttcaa actttaaaga tgaagaaatt 420

actgagcaac aagaagatgg atcaggtgtc atggagttac ttcaagttgt agatattgt 480

tccaaacgtcg aagatccaca gtgttgccgc ttgtatgctg ctgatatata tgacaacata 540

catgttgcag agttcaaca acgacccttg gctaattata tggagcttgc gcagcgagat 600

atcgacccag acatgagaaa gattctgatt gactggcttg tagaagtttc tgacgactac 660

aagctggttc cagatacgt ttaccttaca gtgaatctta tcgaccgggt tctgtccaa 720

agttacattg aaaggcaaag actccagctc cttgggtctt cttgcattgtc tatacgat 780

aaatatgaag agcttccgc accaggggtg gaggagttt gcatttcattac ggccaacaca 840
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ttatcggttc ctaccaccaa aacatttctg aggcggttca ttaaagcagc tcaagcttcg 960
tacaagggtgc ctttcattga actggagttat ttagcaaact atctcgccga attgacactg 1020
gtgaaatata gtttcctaag gttcctgccca tcactaattt ctgcttcagc tgtttccta 1080
gccccatgga cactcgacca aactgaccat ctttggaaacc ctactctgca acactacacc 1140
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<210> 2
<211> 436
<212> PRT
<213> *Arabidopsis thaliana*

<220>
<221> MISC_FEATURE
<223> A variant of the sequence deposited under accession number
NP_568248 contains an arginine instead of a proline on position
284 and a phenylalanine instead of a serine on position 432

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Met Tyr Cys Ser Ser Ser Met His Pro Asn Ala Asn Lys Glu Asn Ile
1 5 10 15

Ser Thr Ser Asp Val Gln Glu Ser Phe Val Arg Ile Thr Arg Ser Arg
20 25 30

Ala Lys Lys Ala Met Gly Arg Gly Val Ser Ile Pro Pro Thr Lys Pro
35 40 45

Ser Phe Lys Gln Gln Lys Arg Arg Ala Val Leu Lys Asp Val Ser Asn
50 55 60

Thr Ser Ala Asp Ile Ile Tyr Ser Glu Leu Arg Lys Gly Gly Asn Ile
65 70 75 80

Lys Ala Asn Arg Lys Cys Leu Lys Glu Pro Lys Lys Ala Ala Lys Glu
85 90 95

Gly Ala Asn Ser Ala Met Asp Ile Leu Val Asp Met His Thr Glu Lys
100 105 110

Ser Lys Leu Ala Glu Asp Leu Ser Lys Ile Arg Met Ala Glu Ala Gln
115 120 125

Asp Val Ser Leu Ser Asn Phe Lys Asp Glu Glu Ile Thr Glu Gln Gln
130 135 140

Glu Asp Gly Ser Gly Val Met Glu Leu Leu Gln Val Val Asp Ile Asp
145 150 155 160

Ser Asn Val Glu Asp Pro Gln Cys Cys Ser Leu Tyr Ala Ala Asp Ile
165 170 175

Tyr Asp Asn Ile His Val Ala Glu Leu Gln Gln Arg Pro Leu Ala Asn
180 185 190

Tyr Met Glu Leu Val Gln Arg Asp Ile Asp Pro Asp Met Arg Lys Ile
195 200 205

Leu Ile Asp Trp Leu Val Glu Val Ser Asp Asp Tyr Lys Leu Val Pro
210 215 220

Asp Thr Leu Tyr Leu Thr Val Asn Leu Ile Asp Arg Phe Leu Ser Asn
225 230 235 240

Ser Tyr Ile Glu Arg Gln Arg Leu Gln Leu Leu Gly Val Ser Cys Met
245 250 255

Leu Ile Ala Ser Lys Tyr Glu Glu Leu Ser Ala Pro Gly Val Glu Glu
260 265 270

Phe Cys Phe Ile Thr Ala Asn Thr Tyr Thr Arg Pro Glu Val Leu Ser
275 280 285

Met Glu Ile Gln Ile Leu Asn Phe Val His Phe Arg Leu Ser Val Pro
290 295 300

Thr Thr Lys Thr Phe Leu Arg Arg Phe Ile Lys Ala Ala Gln Ala Ser
305 310 315 320

Tyr Lys Val Pro Phe Ile Glu Leu Glu Tyr Leu Ala Asn Tyr Leu Ala

325

330

335

Glu Leu Thr Leu Val Glu Tyr Ser Phe Leu Arg Phe Leu Pro Ser Leu
 340 345 350

Ile Ala Ala Ser Ala Val Phe Leu Ala Arg Trp Thr Leu Asp Gln Thr
 355 360 365

Asp His Pro Trp Asn Pro Thr Leu Gln His Tyr Thr Arg Tyr Glu Val
 370 375 380

Ala Glu Leu Lys Asn Thr Val Leu Ala Met Glu Asp Leu Gln Leu Asn
 385 390 395 400

Thr Ser Gly Cys Thr Leu Ala Ala Thr Arg Glu Lys Tyr Asn Gln Pro
 405 410 415

Lys Phe Lys Ser Val Ala Lys Leu Thr Ser Pro Lys Arg Val Thr Ser
 420 425 430

Leu Phe Ser Arg
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 <212> DNA
 <213> Oryza sativa

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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcatattac	180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgttttatt	240
attgaaatttata tataattcaa agagaataaa tccacatagc cgtaaagtcc tacatgtgg	300
gcattaccaa aatatataata gcttacaaaa catgacaaggc tttagttgaa aaattgcaat	360
ccttattcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgtcaccc	420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag	480
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt	540
aaaactaaca ctctaaagca accgatggaa aagcatctat aaatagacaa gcacaatgaa	600

aatcctcatc atcttcacc acaattcaa tattatagtt gaagcatagt agta 654

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<212> DNA
<213> Artificial sequence

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<223> primer PRM582

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<210> 5
<211> 52
<212> DNA
<213> Artificial sequence

<220>
<223> primer PRM583

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